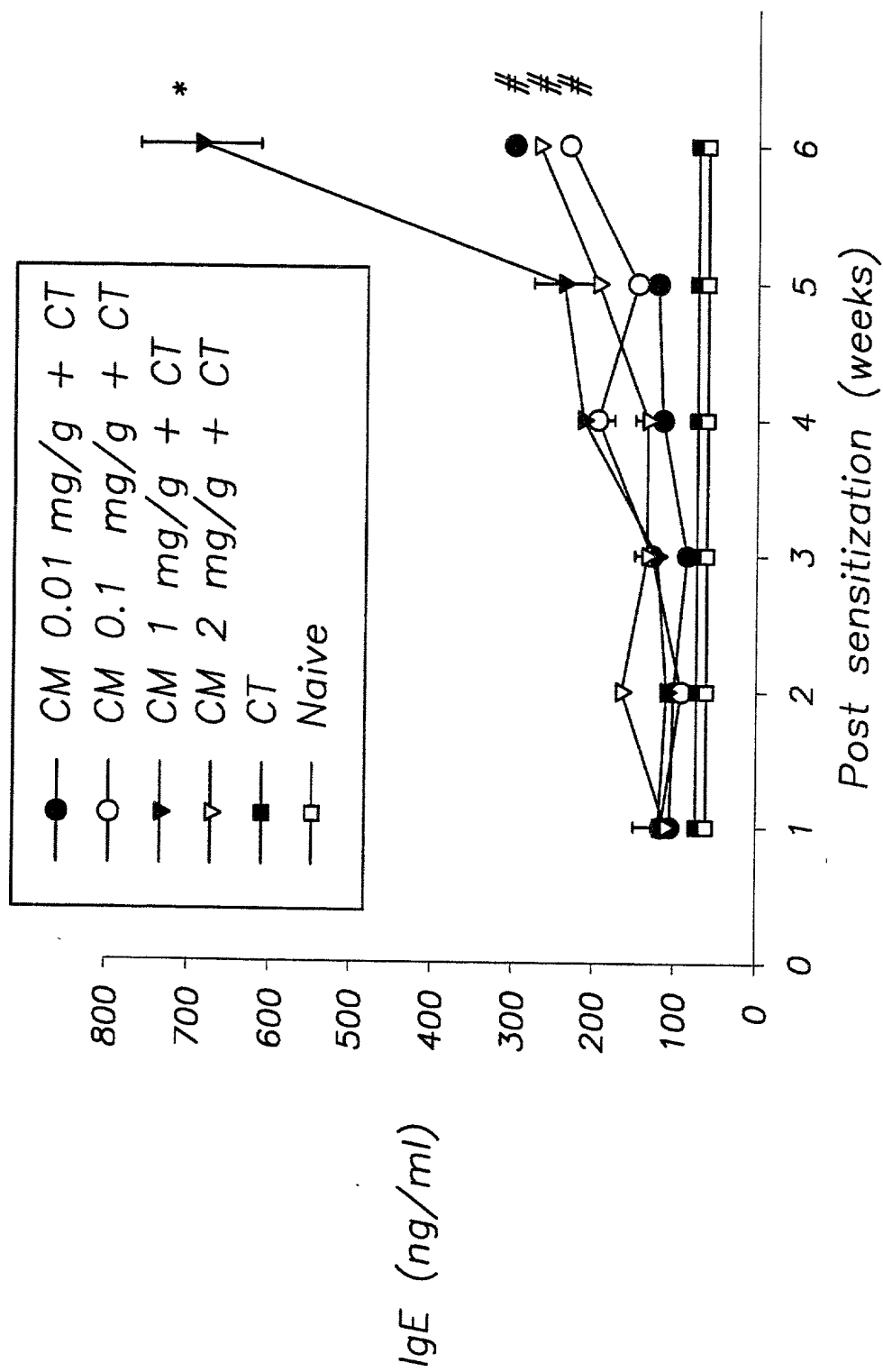


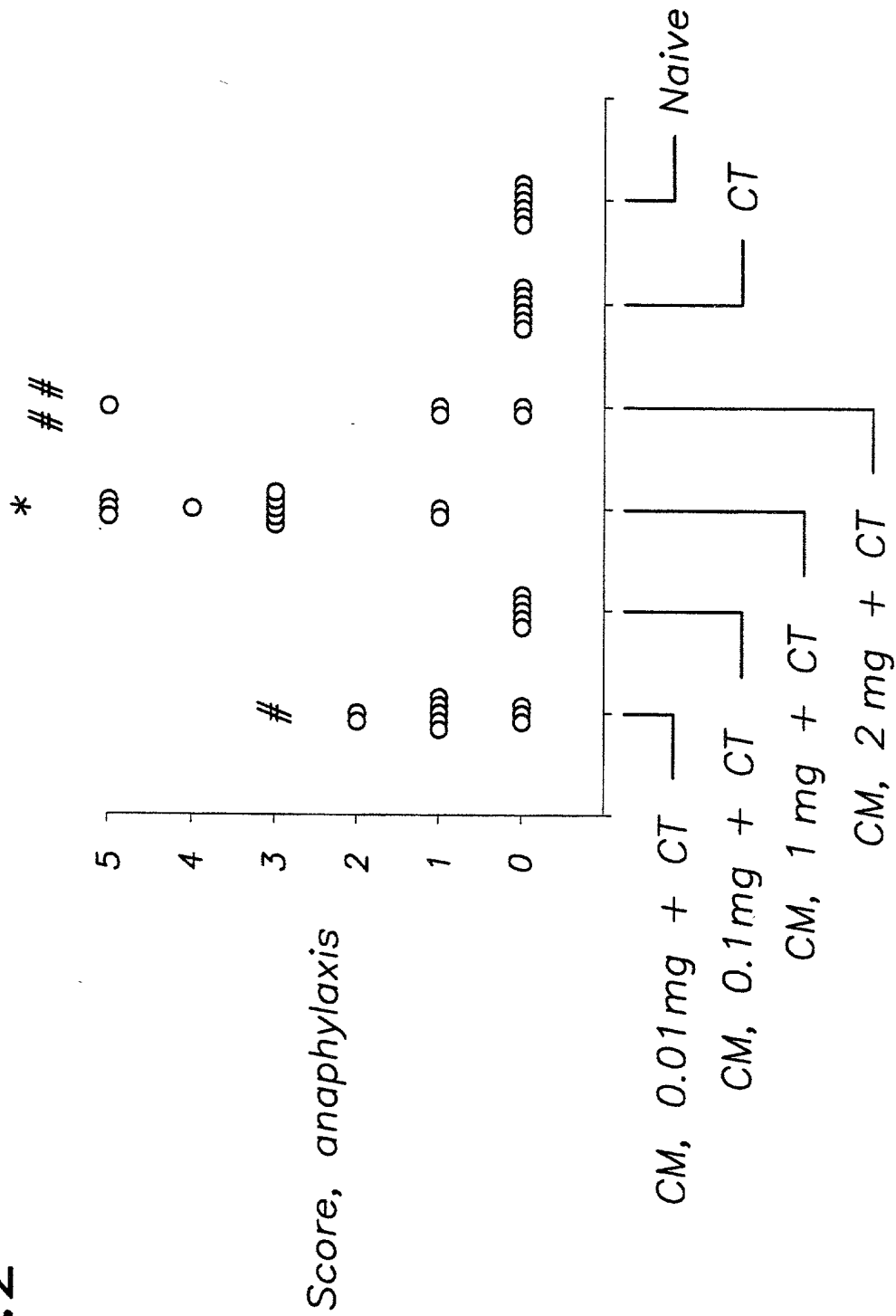
FIG. 1



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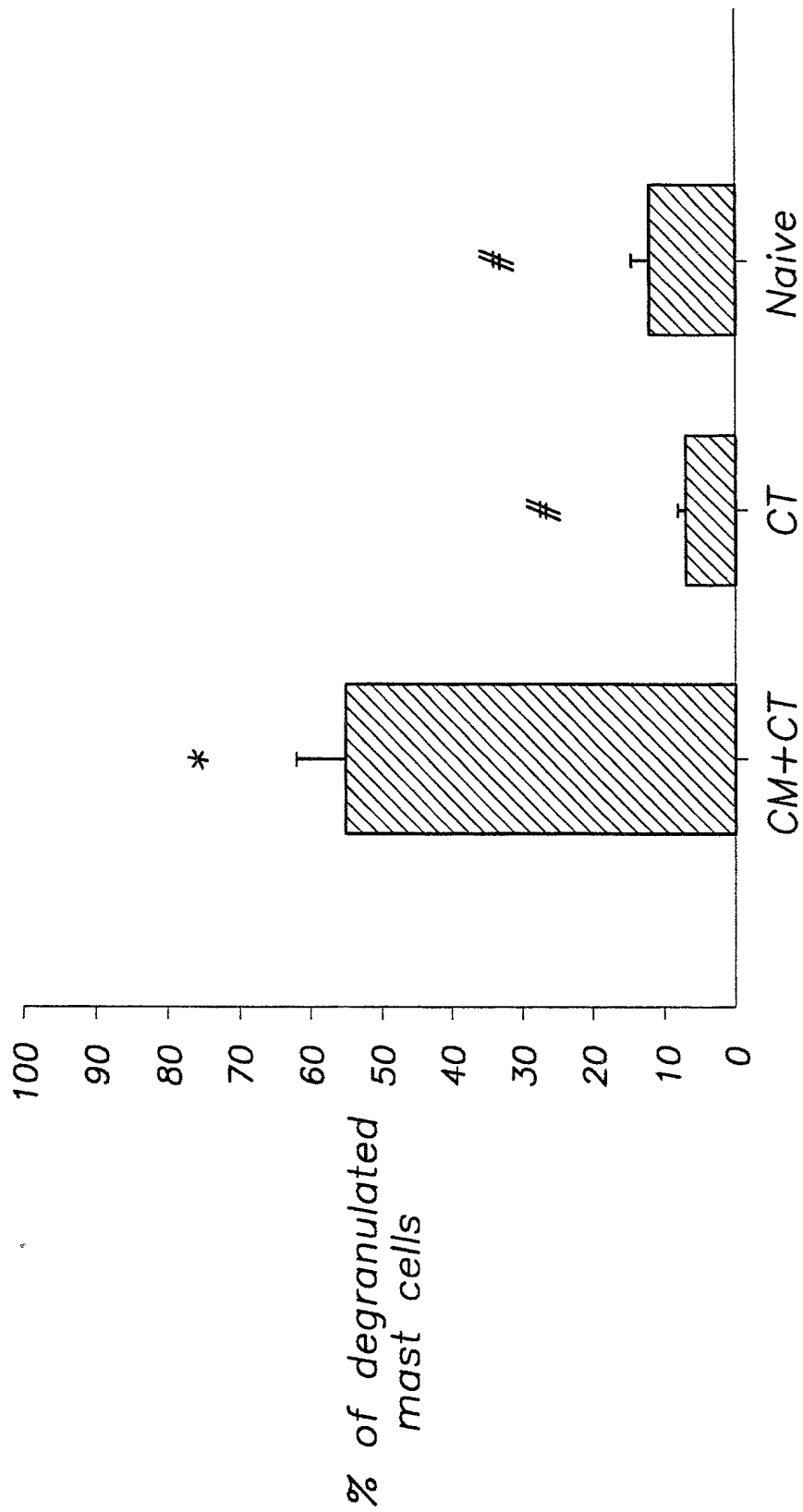
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FIG.2



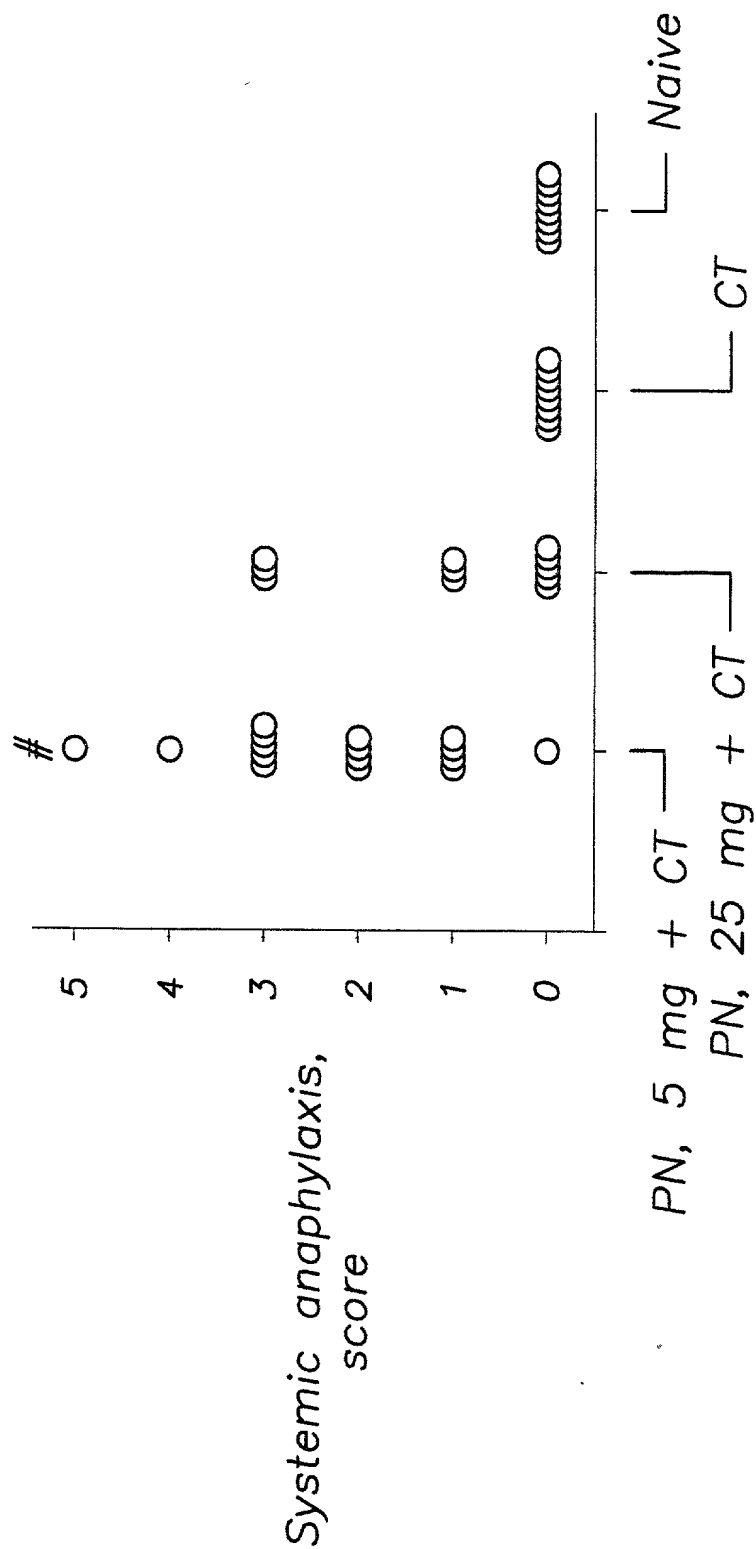
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FIG. 3



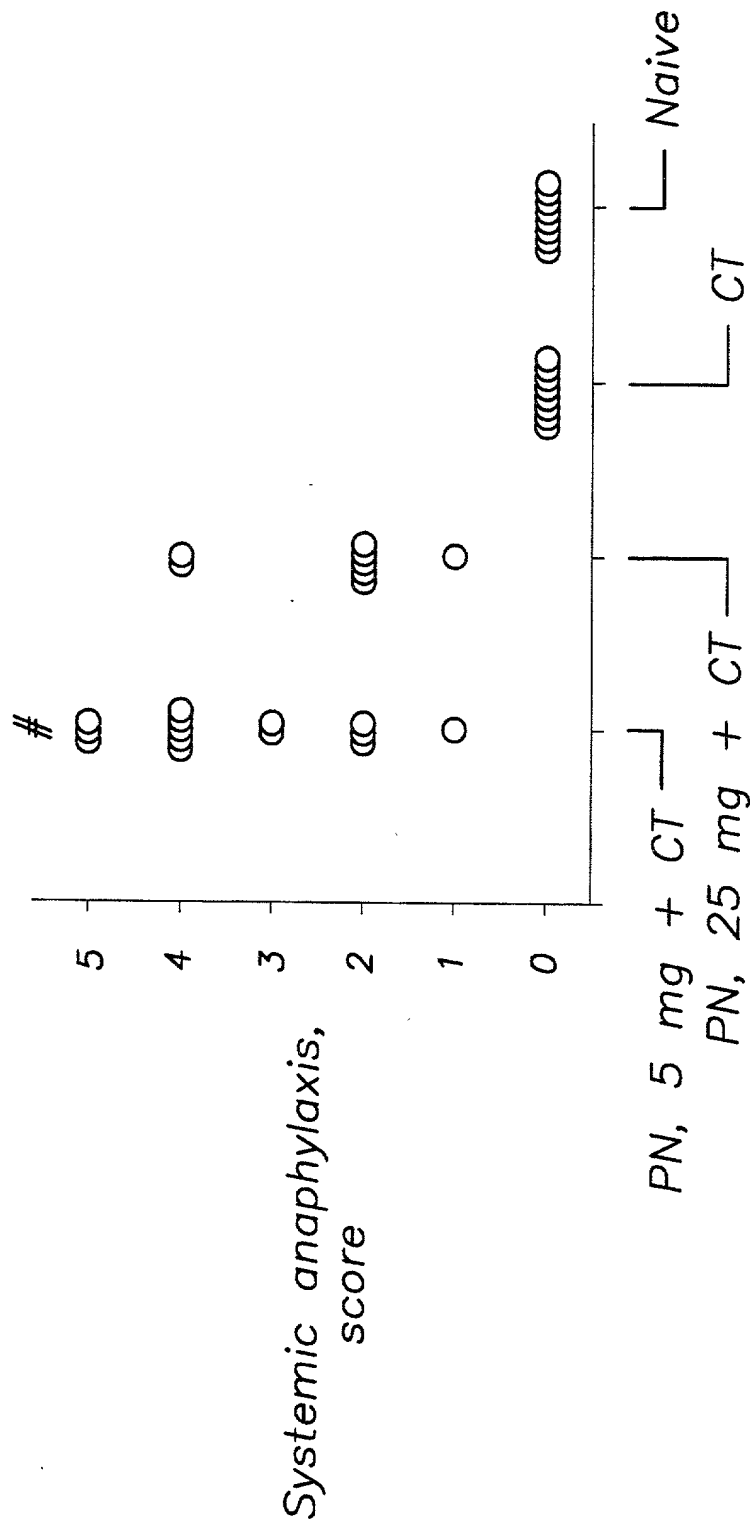
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FIG. 4A (Week 3, first challenge)



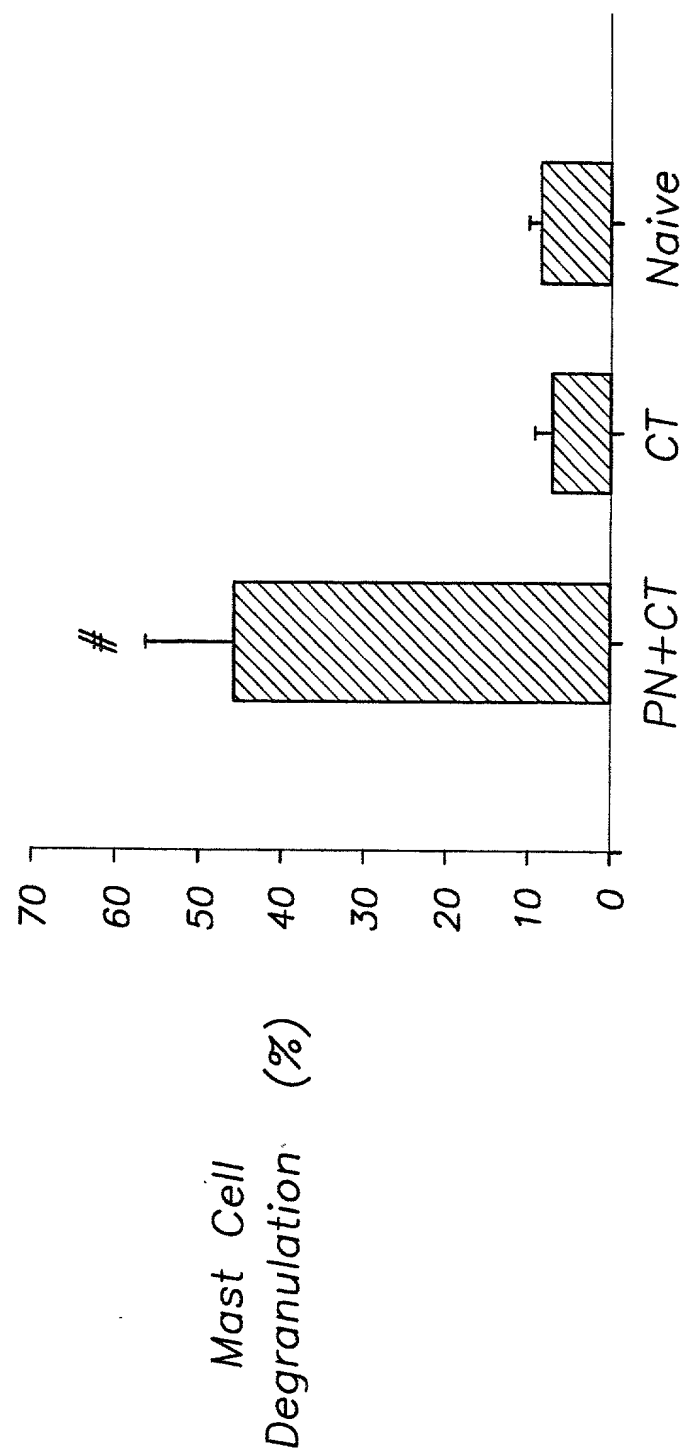
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FIG. 4B (Week 5, re-challenge)



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FIG. 5A



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FIG.5B

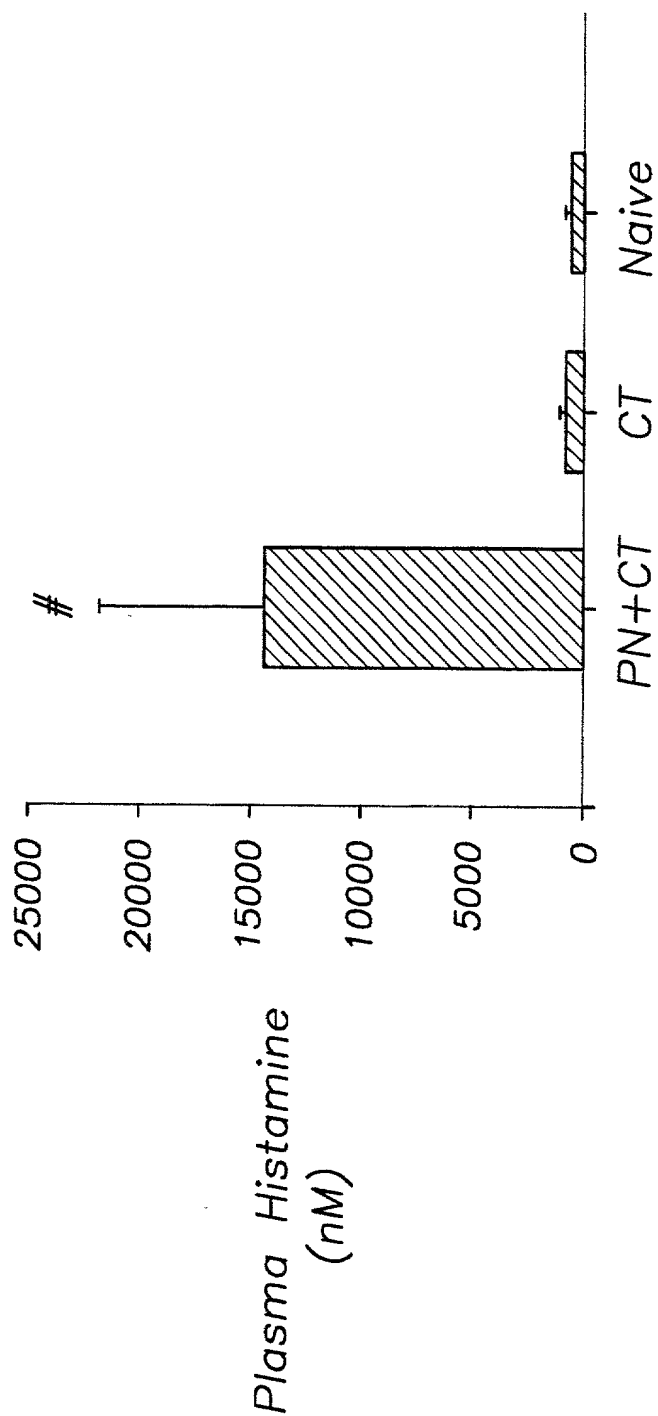
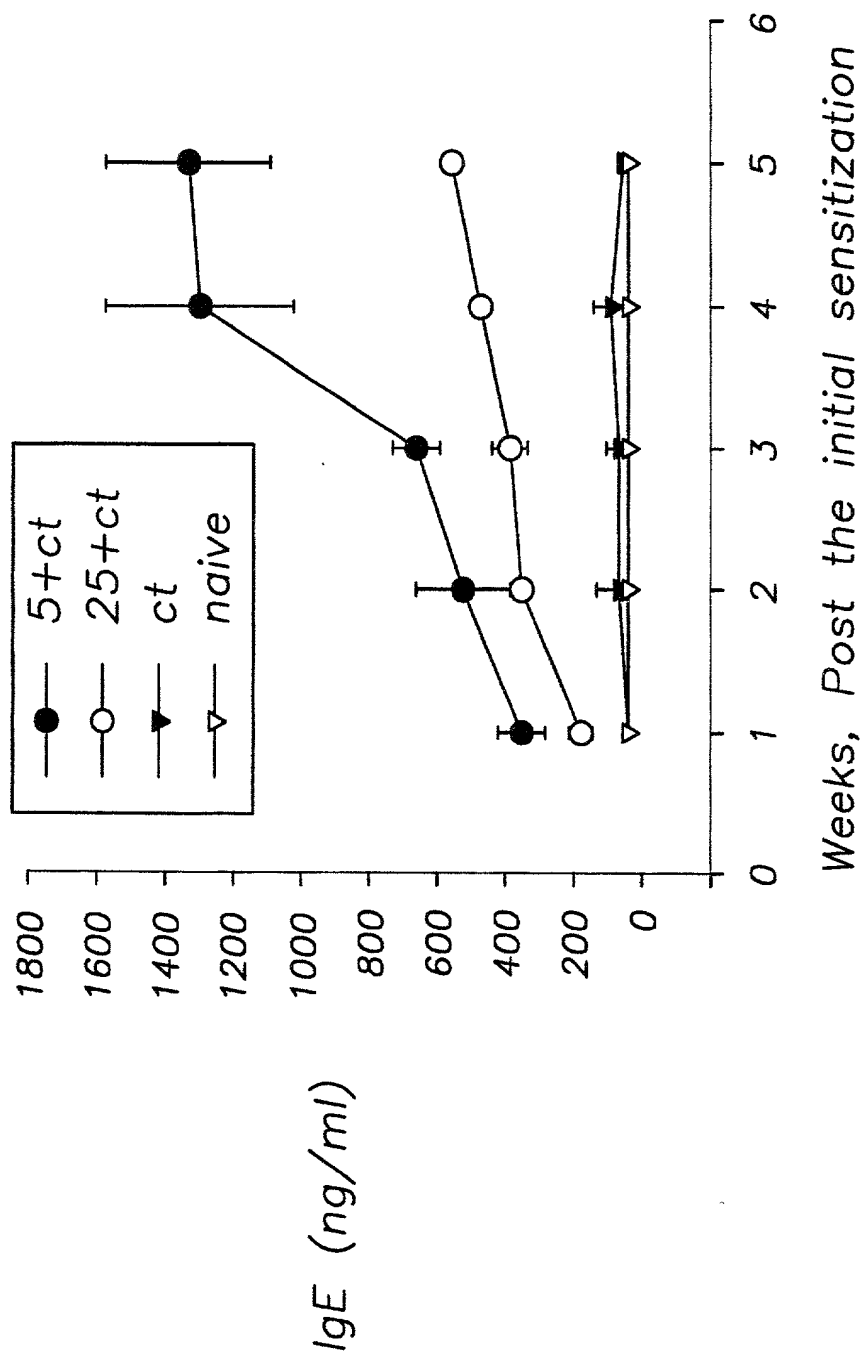
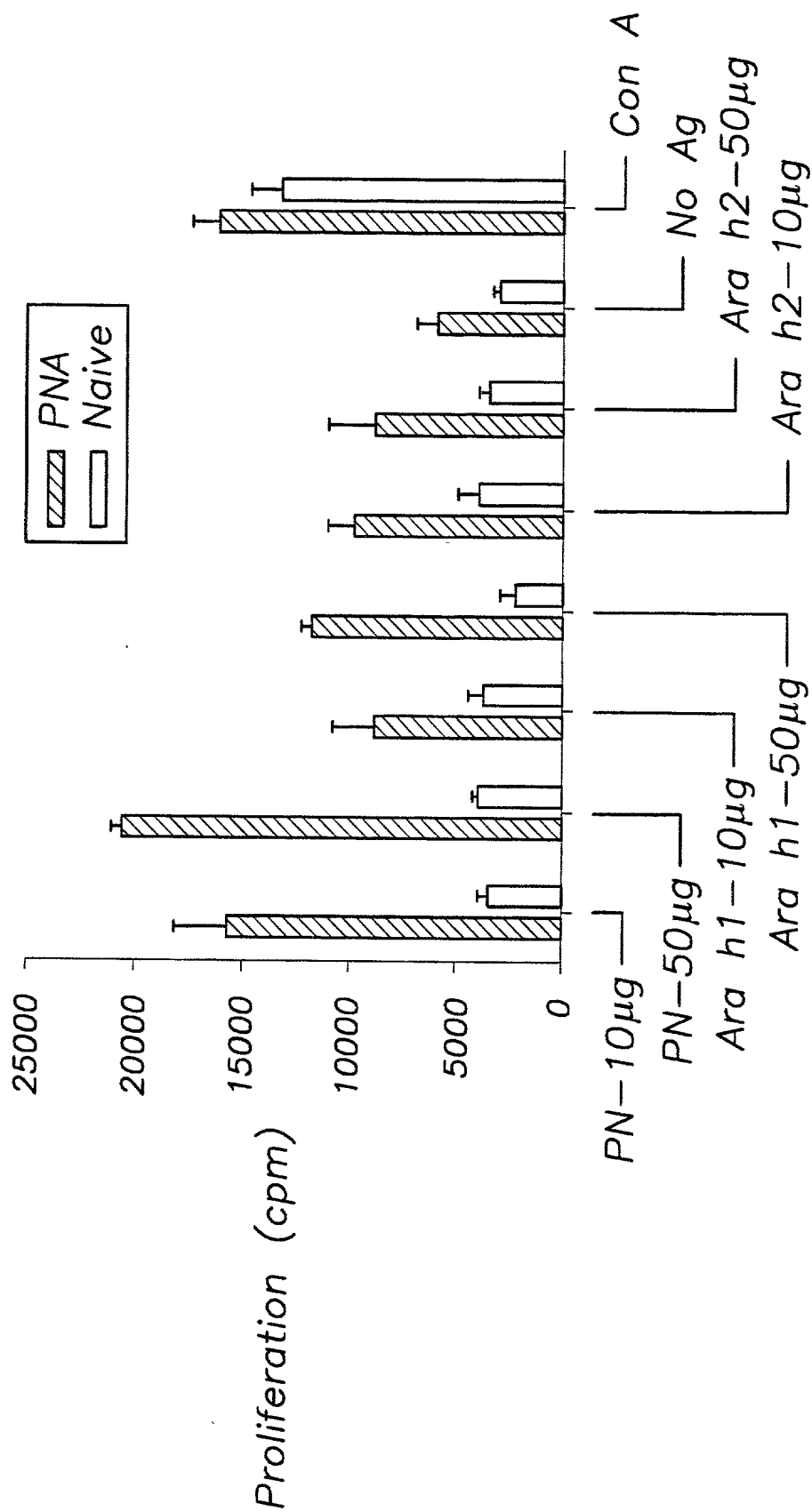


FIG. 6



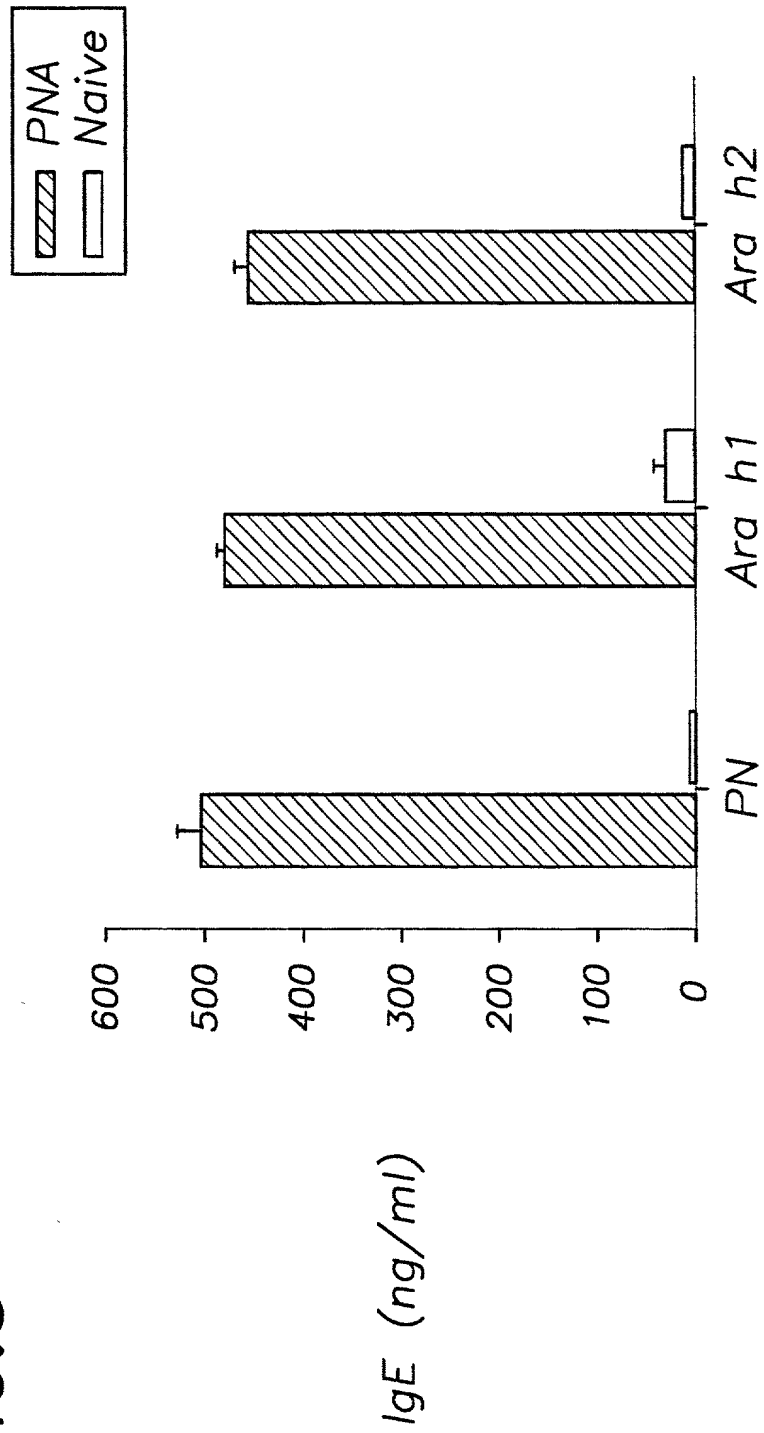
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FIG. 7



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FIG. 8



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FIG.9A

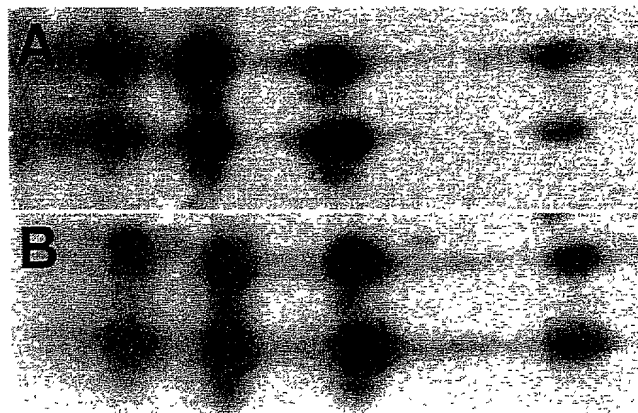


FIG.9B

FIG. 10A

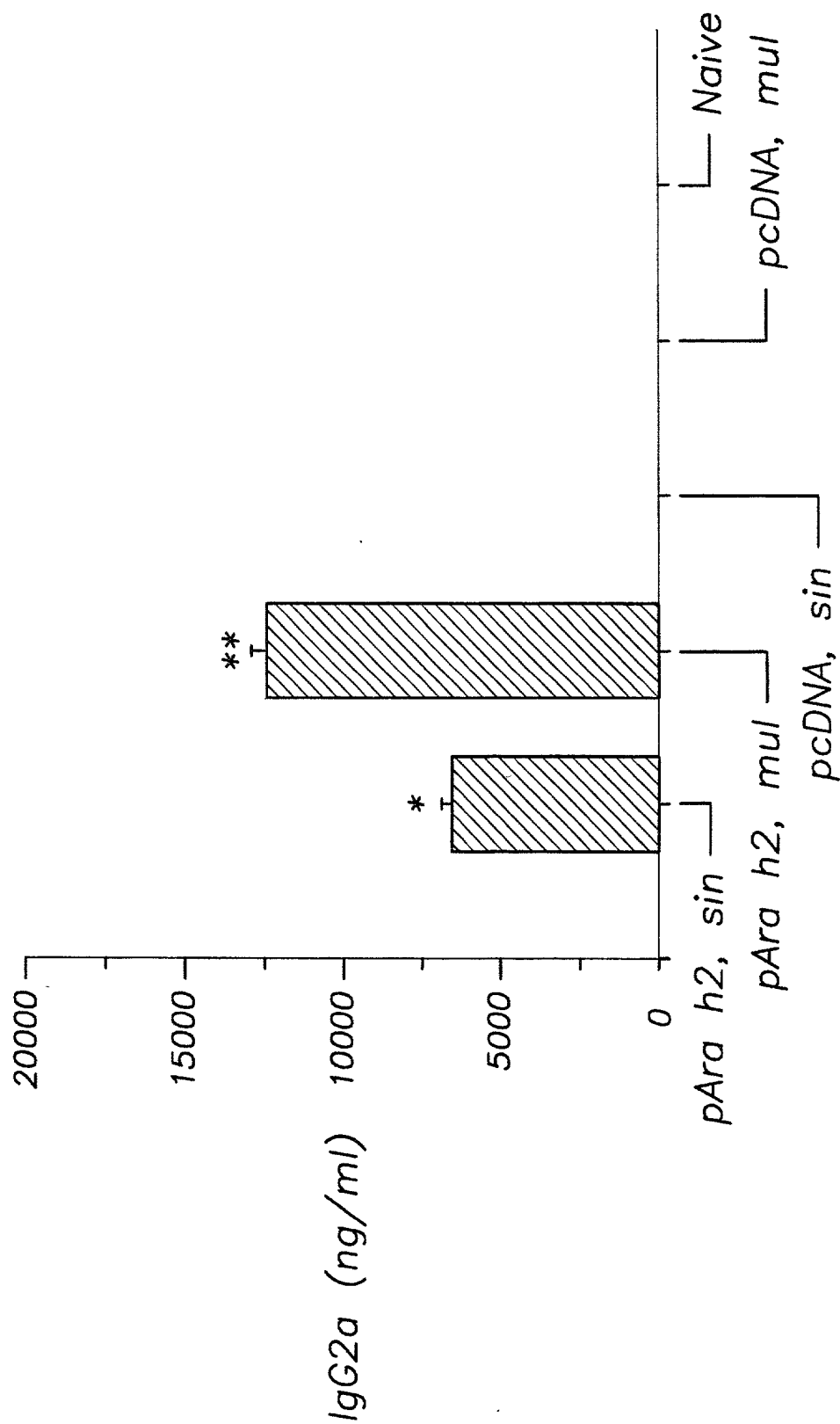


FIG. 10B

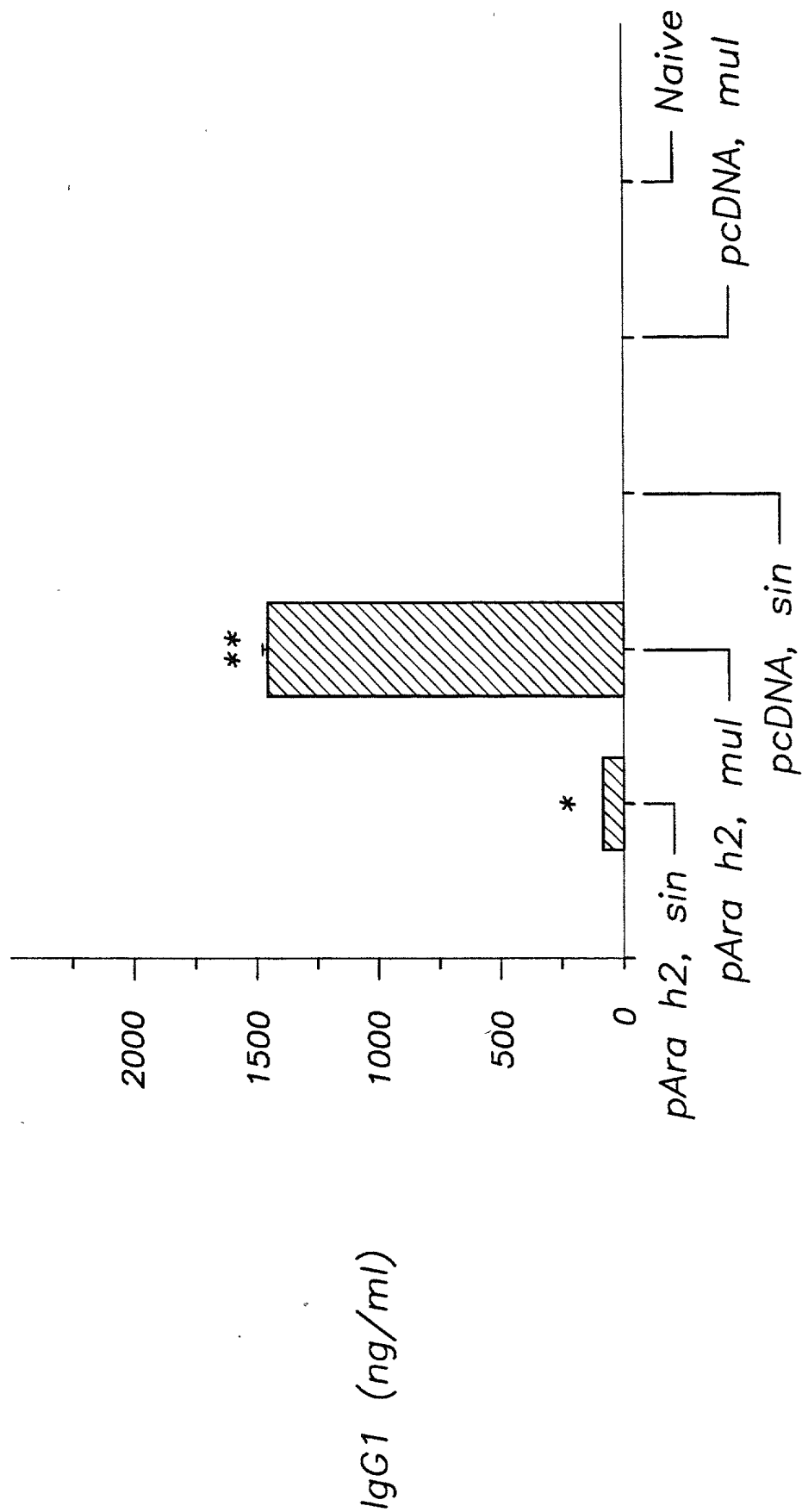


FIG. 11

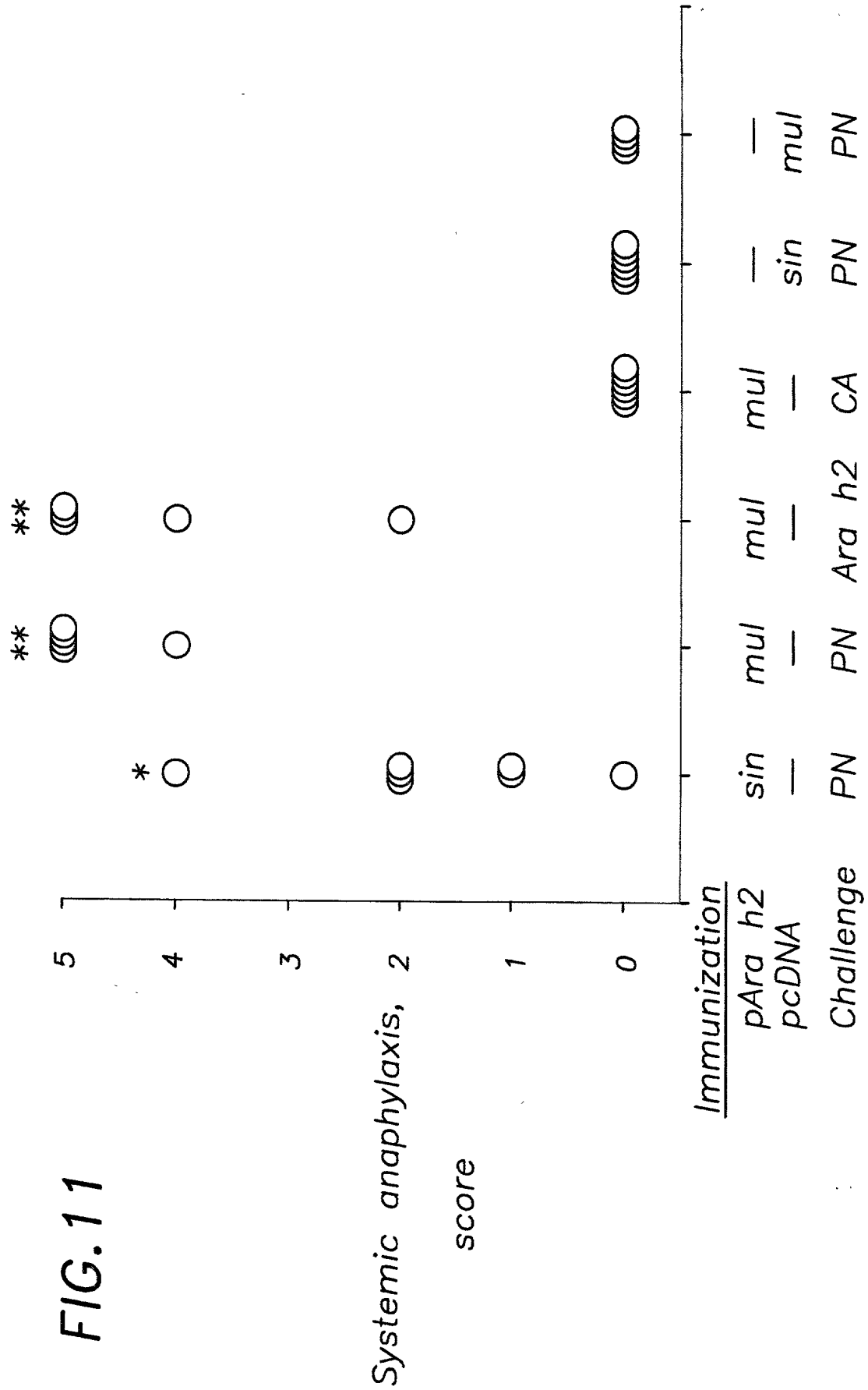


FIG. 12

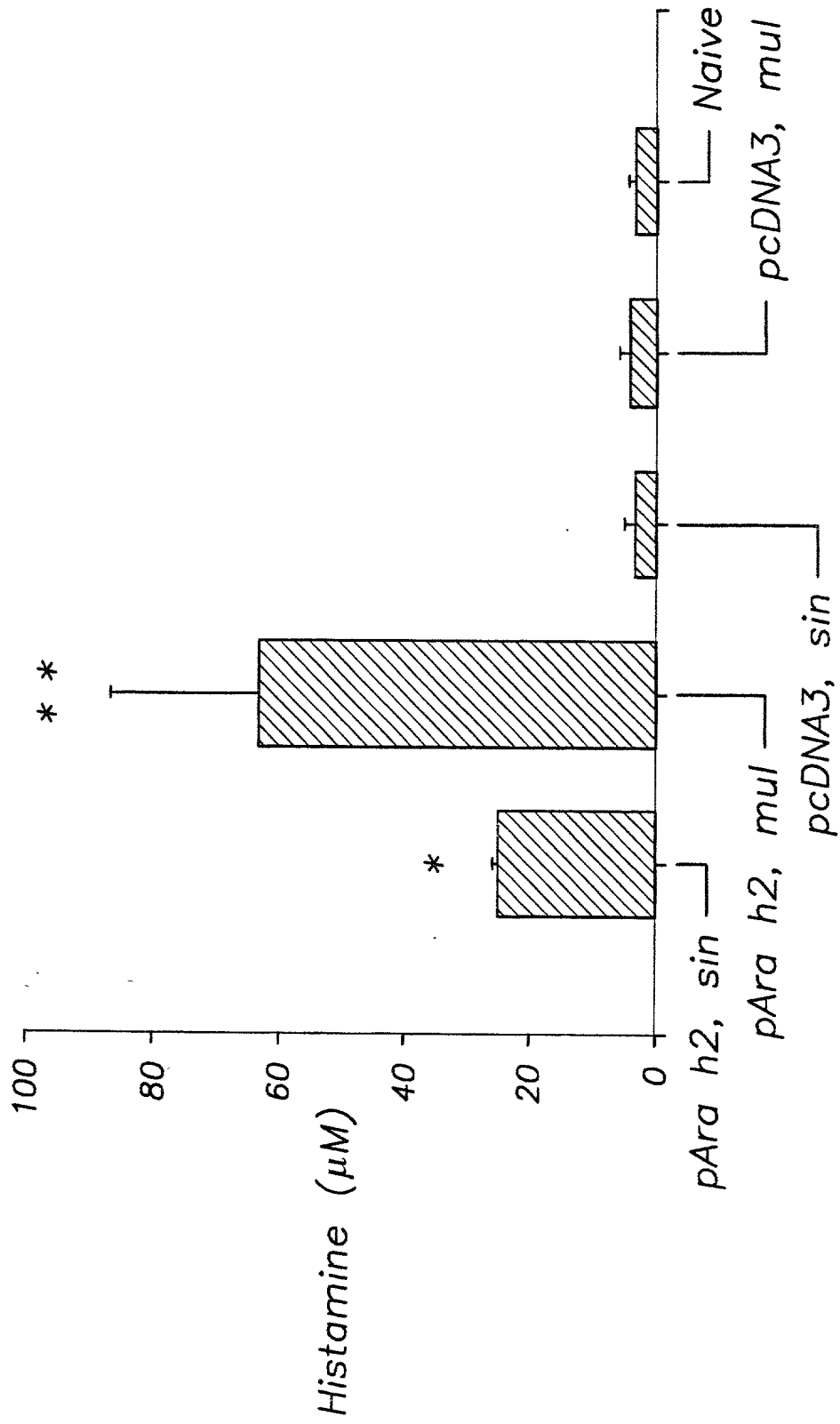


FIG. 13

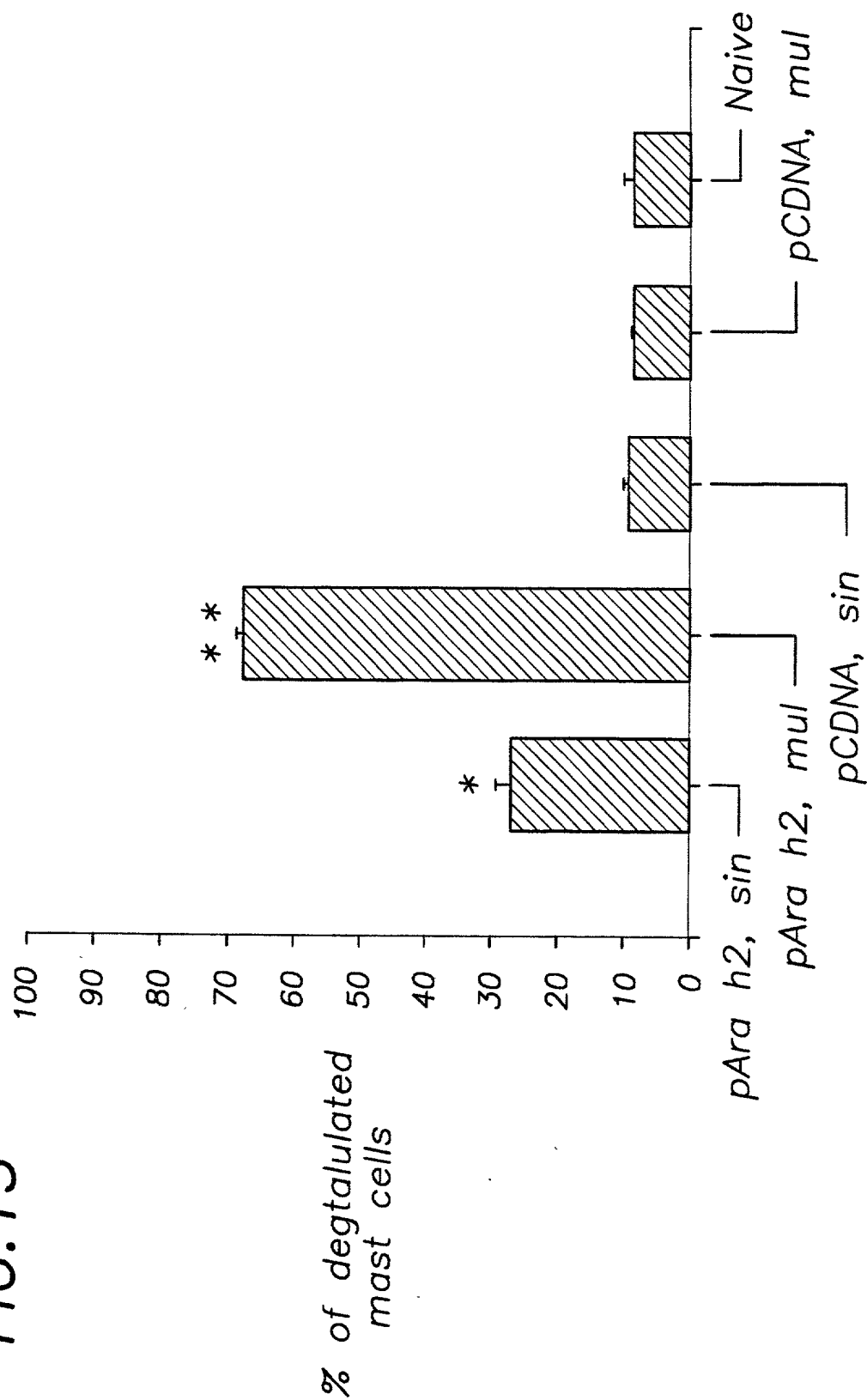


FIG. 14A

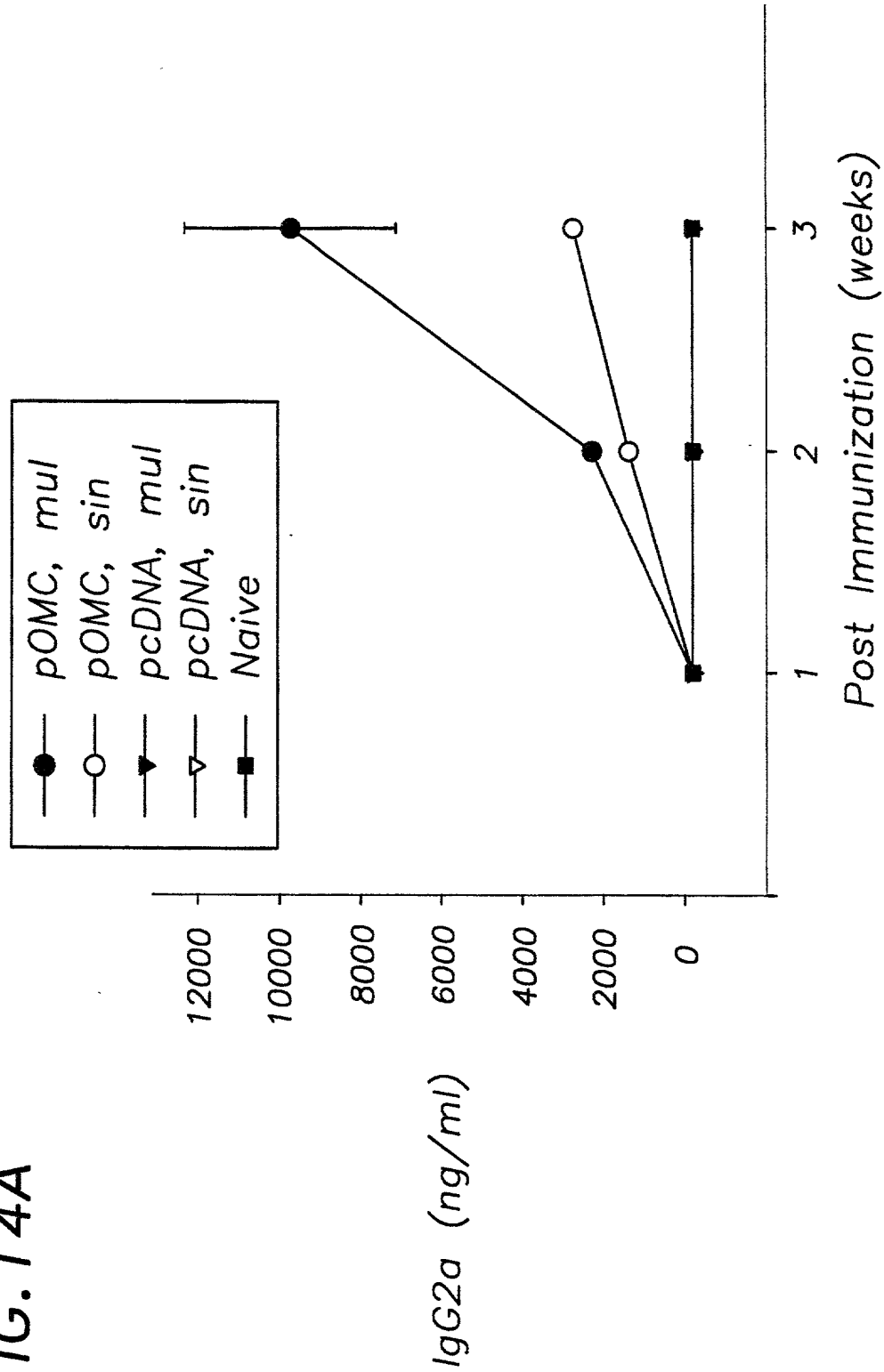
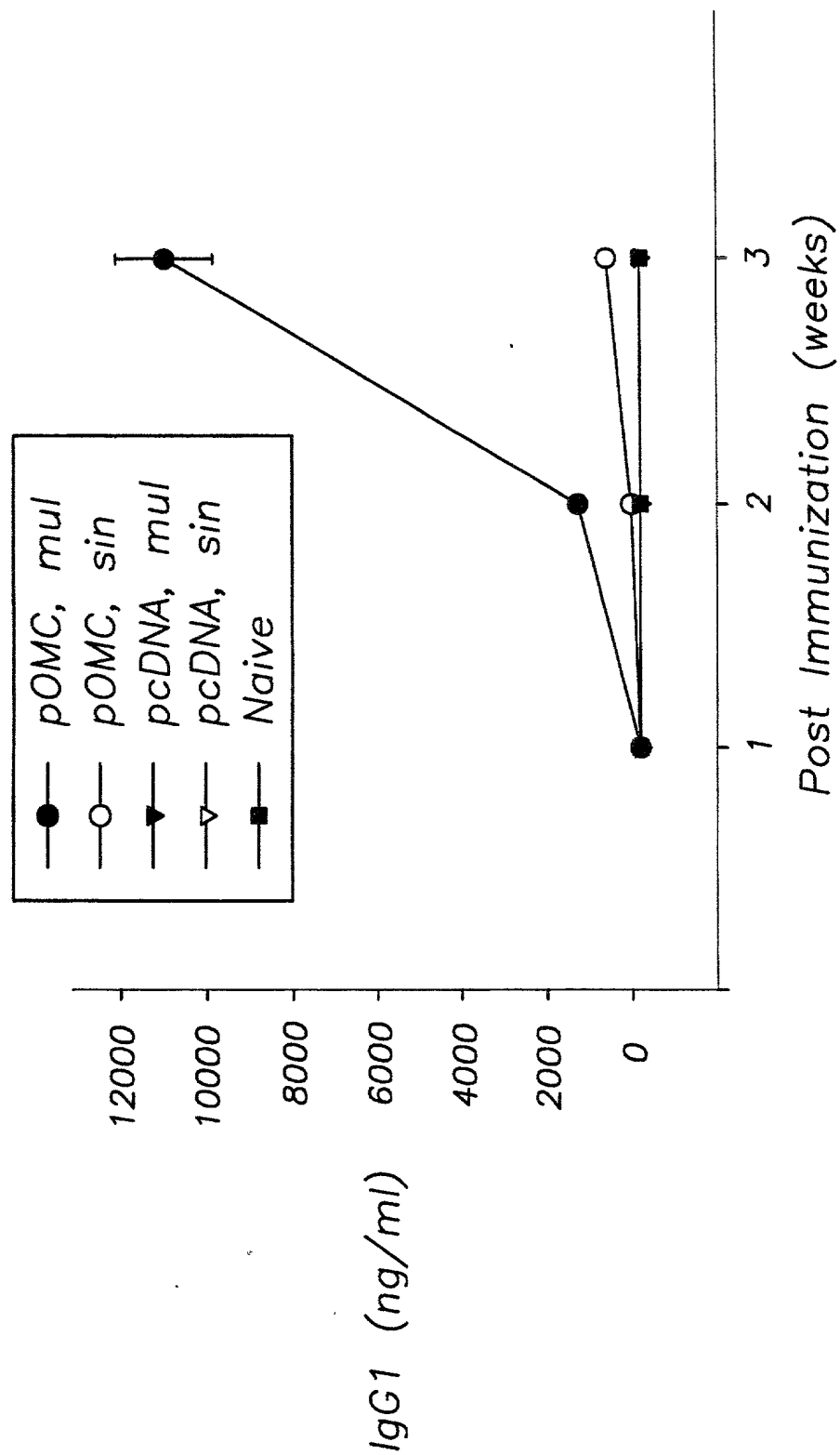


FIG. 14B



—●— C3H, pAra h2
—○— C3H, pcDNA
—▼— AKR, pAra h2
—▽— AKR, pcDNA
—■— Balb/C, pAra h2
—□— Balb/C, pcDNA

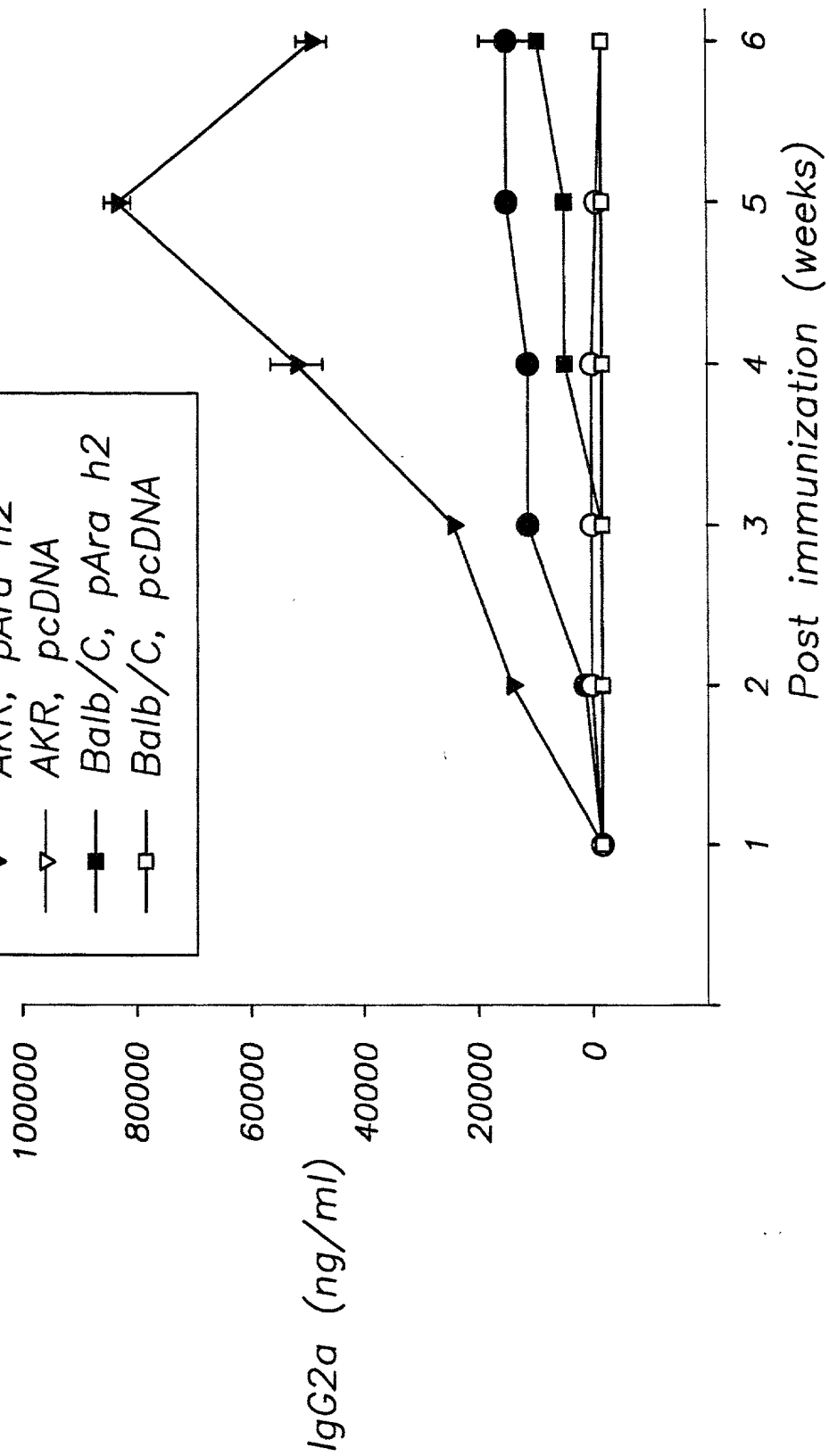


FIG. 15B

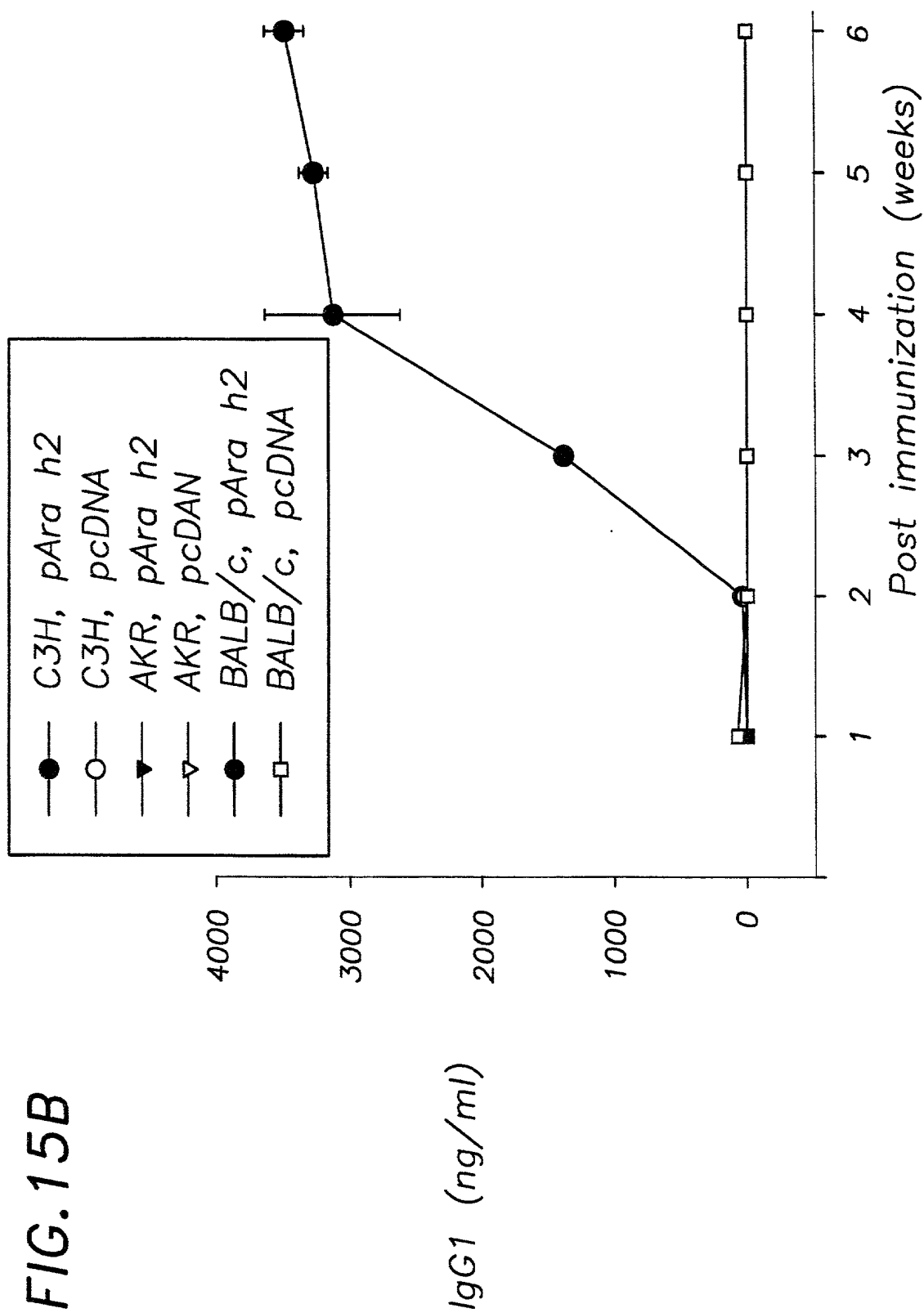


FIG. 16A

PEPTIDE →	Ara h	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10
PATIENT 1	5.3	0.9	2.9	3.8	7.8	0.9	0.9	0.7	1	0.9	0.7
PATIENT 2	4.3	0.7	1.4	1.3	2.4	0.9	0.8	0.7	0.7	1	0.7
PATIENT 3	2.8	1	1.8	1.6	2.4	1.1	1.1	1.4	1.7	1.3	1.3
PATIENT 4	1.8	1	0.6	0.8	2.1	1	0.5	0.7	1.4	0.7	0.8
PATIENT 5	5.5	2.1	1.1	0.7	0.8	1	1.3	0.7	1.5	0.5	0.6
PATIENT 6	20.8	1	1.6	2.2	1.7	1.4	1	1.8	2.7	2.6	1.2
PATIENT 7	1.5	0.7	0.5	0.7	0.9	0.9	0.7	0.9	1.1	0.8	0.7
PATIENT 8	6.5	2.4	1.2	1.3	1.1	0.9	1.1	1.4	0.8	0.9	0.8
PATIENT 9	9.2	1.1	1.1	6.3	1.2	1.5	1.2	1	1.2	1.3	0.8
PATIENT 10	11.7	0.7	0.6	0.7	0.6	1.3	0.5	0.6	0.9	0.6	0.5
PATIENT 11	2.1	0.7	0.7	0.5	0.6	0.5	0.3	0.6	0.5	0.5	0.5
PATIENT 12	1.1	1.4	1.6	1.8	2.8	1.5	1.5	1.4	1.3	1.5	1.2
PATIENT 13	0.9	1.3	1.9	1.9	2.8	2	1.6	2.4	1.9	1.5	1.5
PATIENT 14	4.8	1.2	1.6	1.5	1.9	1.6	1.9	1.3	1.6	1.8	1.3
PATIENT 15	6.9	0.7	1.1	1.8	2.1	1.1	1	1.1	1.1	1	0.8
PATIENT 16	10.2	0.7	1.6	2.7	10.9	2	0.9	2.1	2.1	1.4	1
PATIENT 17	4.2	1.4	1.6	2.8	2.6	1.3	1.4	1.7	1.6	1.1	1.3
PATIENT 18	3.9	1.5	1.7	2.9	3.3	1.5	1.2	1.3	1.3	1.9	1
PATIENT 19	3.4	1.5	1.2	2.6	1.4	1.7	0.9	1	1.4	1.2	1.1

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TO
FIG. 16B

FIG. 16B

#11	#12	#13	#14	#15	#16	#17	#18	#19	#20	#21
0.9	1	0.8	1.2	0.9	1	1.2	1	5	7.3	6.6
0.7	0.6	0.5	1.1	0.7	0.7	0.7	0.5	1.9	4.3	3.4
1.7	0.9	0.9	1.3	1.2	1.4	1.2	1.1	1.1	1.4	1.4
0.7	0.5	0.6	1	1	0.7	0.7	0.7	1	1.4	1.6
0.7	0.3	0.8	0.8	0.7	0.5	0.5	0.6	4.4	2.2	1.6
1.4	1.2	1.2	1.1	0.9	0.7	1.4	3.9	0.6	0.7	0.9
1	1	0.7	0.8	1.1	1.1	0.7	1.2	1.2	1.4	1.4
1.2	1.3	1	1.2	1.4	1	1.1	3.5	1.3	1	1.2
0.8	1.5	0.9	0.8	0.9	1.1	0.7	1.9	1.4	1.3	1.4
0.5	0.8	0.7	0.4	0.5	0.7	0.7	0.6	1.6	1.2	1.1
0.8	0.5	0.7	0.7	0.4	0.4	0.7	0.6	0.6	0.5	0.8
1.1	1	1.1	1.4	1.4	1.1	1.3	1.2	1.3	1.9	2
1.7	1.9	1.4	1.2	1.5	1.3	1.5	2.3	1.6	1.3	1.8
1.1	1.3	0.9	0.9	1.2	1.1	1.5	5.1	3.5	2.2	2.1
1	1	1.2	1	0.7	1.2	1.4	2.2	1.2	1.1	1.4
0.8	0.9	0.8	0.6	0.8	0.7	0.7	1.6	3	2.5	5.8
1.2	1.7	1.7	1.1	1.7	1.5	1.6	1.2	1.4	1.2	1.3
1.3	1.2	0.9	1.7	1.7	1	1.6	2.1	3.4	3.8	6.3
1	1.3	1.1	1.4	1.6	1.3	1.3	1.3	1.4	1.5	1.7

FROM
FIG. 16A

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TO
FIG. 16C

FIG. 16C

#22	#23	#24	#25	#26	#27	#28	#29
6	3.4	4.6	6.4	7.5	5.1	11.3	0.9
3.6	1.4	1.4	1.5	1.9	1.5	2.2	0.5
2.1	1.1	0.7	1.2	1.2	1.3	0.9	1.2
2	1.2	1.1	1.4	1.4	1.5	1.1	0.6
* 2.5	1.4	1.7	1.9	2.2	1.7	3.3	0.5
0.8	1	0.7	0.9	0.6	0.7	1	1.5
* 2.3	1.5	1.6	1.3	1.5	1.4	1.8	0.6
1	1.1	1.8	1	1.1	1.5	1.3	1.3
0.5	1.5	1.5	1.2	1.2	1.6	1.1	2
1.3	1.3	0.7	1.5	1.3	1.5	1.4	0.6
0.6	0.6	0.7	0.7	0.8	0.8	0.5	0.5
1.5	1.3	1.3	1.7	1.8	1.1	1.3	1.4
1.6	1.5	1.7	1.6	1.7	2.2	1.3	1.4
1.9	1.6	1.5	2.8	3.3	2	2.7	1.1
1.4	0.9	1.2	1.5	1.5	1.4	1.1	0.9
16.8	1.4	1.7	4.9	3.3	5.3	12.1	1.4
1.7	1.2	1.2	1.9	1.6	1.4	2.9	1.2
7	1.6	1.8	2.7	3.5	4.3	5.1	1.6
2.4	1.4	1.6	1.5	1.3	1.2	1.7	0.9

FROM
FIG. 16B

FIG.17A

Modified Ara h 1:

MASMTGGOMGRDPNSSS THAKSSPYQAKT ENPCAQRCLQSCQCEPDALK
QKACESRCTKLEYDPRCAYD PRGHTGTTNQRSPPGEAT RGQPGDYDDARRQPRAEEGGR
WGPA GPREREREEDARQ PREDWARPSHQ QPRKARPEGREGEQEWGTPGSHVREETSRNNP
FYFPSRRFSTRYGNQNGRI RVLQRFQDRSRQFN LQNHRIVQIEAKPNTLVLPKHADADN
ILVIQQGQATVTVANGNNRKS FNLDGHALRIPSGFI SYILNRHDNQNLRVAKISMPVNT
PGQMEDFFP ASSRDQSSYLQGFARNTLEA AFNAEANEIRRVLLEENAGGEQEARGQRRWS
TRSENNEGVI VKVSKEHVEELTKHAKSVSKKGSEEEGDITNPANL REGEPLSNNFGKL
AEVKPDKKNPQLQDL DMMLTCVEIKEGALMLPHFNSKAMVI VVVKGTGNLELVAVRKEQ
QQRGRREEEDEDEEEEGSNREV RAYTARLKEGDVFI MPAAHPVAINASSELALLGFGIN
AENNHRI FLAGDADNVIDQIEKQAKALAAPGSGEQVEKL KNQKESHFVAARPQSQSQSP
SSPEKESPEKEDQEEENQGGKGPLLSILKAFN KLAAALEHHHHHHH (SEQ ID NO. 109)

FIG.17B

Modified Ara h 2:

MASMTGGOMGRDPNS ARQQAELQGDRRCQSQLARANLRACEHLMQKI Q

AEDSYERAPYSPSQAPYSPSPYDRRGAGSSQHQRCCNELNEFENNQRC

MCEALQQIMENQSDRLQGAQQEQQFKREARNLPQQCGLRA PQRCDADVES

GGRDRY AAALEHHHHH (SEQ ID NO. 108)

FIG.17C

Modified Ara h 3:

M ASFRQQPEENACQFQRLNAQRPDNRIESEG^YIETWNANNQEFECAGV
ALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPRHYEEPHTQGRRSQSQRRPP
RRLQGEDSQQQRDSHQKVHRFDECDLI AVPTGVAFWL YNDHDTDVVAVSLTD TNNNDNQ
LDQFPRRFNLAGNTEQEFLRYQQQSRQRRRSLPSPSPQSPRQEEREFSPRGQHSRR
ERAGQEEENE^GNI FSGFTPEAL FQAFQVDDRQI VQNL RGETESEE^EGA I VTVRGGLRAL
SPDRKRRADEEEEEYDEDEYAYDEEDRRRGRGSRGRNGIEETICTASAKKNIGRNRSPDI
YNPQAGSLKTANDLNLILRWLGPSAEYGNLYRNALFVAHYNTNAHSI IYRLRGRAHVQV
VDSNGNRVYDEELQEGHVLVVPQNFAVAGKQSENFEYVAFKTD^SRP^SI ANLAGENSVID
NLPEEVVANSYGLQREQARQLKNNNPFFKFVPPSQSQSPRAVA VDKLAAL EHHHHHH

(SEQ ID NO. 110)

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